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## Author Correction: Genetic landscape of T cells identifies synthetic lethality for T-ALL

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Correction to: *Communications Biology* (2021) 4:1201; <https://doi.org/10.1038/s42003-021-02694-x>, published online 20 October 2021.

The original version of the Supplementary information associated with this Article contained errors in the oligonucleotide sequences of the morpholinos ZF\_PI4KAA\_ATG and ZF\_POLE\_ATG in Supplementary Table 1. There were also sequencing errors in the forward and reverse sequences of primers for *mat2aa*, *nol9* and *EIF5* in Supplementary Table 4; the tables should have appeared as shown below. The original file has been corrected.

### Supplementary Table 1 | Antisense morpholino oligonucleotides used in this study.

Mutant	Affected Gene	ENSEMBL Gene ID <sup>a</sup>	Name <sup>b</sup>	Sequence	Reference
JM087	<i>anapc1</i>	ENSDARG00000075687	ZF_ANAPC1_ATG	TGTACCACTTGACCAGCACTTTCAT	This study
JM087	<i>anapc1</i>	ENSDARG00000075687	ZF_ANAPC1_ACC5	CTTCATAGACGTGCGACATGAGTTC	This study
HU319	<i>atad5a</i>	ENSDARG00000070568	ZF_ATAD5A_ATG	GGCAATGCAACAACCCAGCCATCT	This study
HU319	<i>atad5a</i>	ENSDARG00000070568	ZF_ATAD5A_DON3	AGAAGTGTGATCTTACCTGATAGG	This study
JM052	<i>fcf1</i>	ENSDARG00000102333	ZF_FCF1_DON2	AAGACTCAAACCTTACATTTCTTGTT	This study
JM052	<i>fcf1</i>	ENSDARG00000102333	ZF_FCF1_ATG	ATGACGGCTGAATTTGTTCGAGATT	This study
JZ061	<i>fli1a</i>	ENSDARG00000054632	ZF_FLI1A_ATG	CGCCTCCTTAATAGTTCCTCCATT	This study
JZ061	<i>fli1a</i>	ENSDARG00000054632	ZF_FLI1A_DON7	TTGGAGAGCCTGAGAAATGGAAAGA	This study
KL069	<i>gemin5</i>	ENSDARG00000079257	GEMIN5ATG	GATGTCTTTCGTGCATTATATACCG	20
KL069	<i>gemin5</i>	ENSDARG00000079257	ZF_GEMIN5_DON4	GCACAAAACCTCTAGTTTACCTGCA	20
KL069	<i>gemin5</i>	ENSDARG00000079257	ZF_GEMIN5_ACC9	ATGCCAACTGTAAGAAAAGTGTGGA	20
18_10	<i>lsm8</i>	ENSDARG00000091656	ZF_LSM8_ACC4	CGATCACAGCCCTTAAACACAAAAT	20
18_10	<i>lsm8</i>	ENSDARG00000091656	ZF_LSM8_ACC3	CGTCCCCTAAAAACAGCACAAAGTCA	20
HY062	<i>mat2aa</i>	ENSDARG00000040334	ZF_MAT2AA_ATG	AGCCGTTTCAGTTGTCCGTTTCATATT	This study
HY062	<i>mat2aa</i>	ENSDARG00000040334	ZF_MAT2AA_ACC4	ACCCTTAAAGTACAACACAGGGATT	This study
IG335	<i>mcm10</i>	ENSDARG00000045815	ZF_MCM10_ACC4	TCTGAAGAGGCTGATTTACATAAGA	This study
JI073	<i>naa50</i>	ENSDARG00000027825	ZF_NAA50_ACC2	CCGGCTACTAGAACAAAAGCAGAAT	This study
JI073	<i>naa50</i>	ENSDARG00000027825	ZF_NAA50_DON2	AGCGTTGTTACATACCTAGCTTGGC	This study
IT429	<i>nek7</i>	ENSDARG00000056966	ZF_NEK7_DON8	GATGGGTTTCTATACCTTACCTCAT	This study
IT429	<i>nek7</i>	ENSDARG00000056966	ZF_NEK7_ATG	CGTCCATTGTGACAGCAGCAGTCGC	This study
HP327	<i>nol9</i>	ENSDARG00000077751	ZF_NOL9_ACC4	AGCACTATATTTACCGAGTTGAGGC	This study
HP327	<i>nol9</i>	ENSDARG00000077751	ZF_NOL9_ATG (3RD_1)	GCTGACCCCCAACGAGACTATAAAC	This study
HG002	<i>pi4kaa</i>	ENSDARG00000076724	ZF_PI4KAA_ACC22	AGCTCAGCCTGAAACAGCAAATGT	This study
HG002	<i>pi4kaa</i>	ENSDARG00000076724	ZF_PI4KAA_ATG	ACGTCCCTCTCGACGACATTATTCA	This study
IG447	<i>pip5k1ba</i>	ENSDARG00000044295	ZF_PIP5K1BA_DON5	TTGTGGATTGIGTGGCTCACCATGT	This study
IG447	<i>pip5k1ba</i>	ENSDARG00000044295	ZF_PIP5K1BA_ATG	GCTCATCTGCCGTTGCACTCATCTT	This study
JI065	<i>pnrc1</i>	ENSDARG00000043904	ZF_PNRC1_ACC2	GGCTGCTTTAGACAAACATGAAACA	This study
JI065	<i>pnrc1</i>	ENSDARG00000043904	ZF_PNRC1_ATG	GACGACCAAAGCATCGCCCAACAT	This study
HG010	<i>pole1</i>	ENSDARG00000058532	ZF_POLE_ATG	GTCTGAAGACTTTCAAATCAGTTAC	20
HG010	<i>pole1</i>	ENSDARG00000058533	ZF_POLE_ACC17	ATCACACACCTGAAACAGGAAAAAT	20
HG010	<i>pole1</i>	ENSDARG00000058533	ZF_POLE_DON13	GATGAAAATTAGACCTGTGGTTCT	20
KW059	<i>snapc3</i>	ENSDARG00000101474	ZF_SNAPC3_ATG	TCTTTGCGTATCTCCGCCATAATTC	20

KW059	<i>snpc3</i>	ENSDARG00000101474	ZF_SNAPC3_ACC7	ATTACCCTTCAGCAAGAACACATAT	20
KH025	<i>EIF5</i>	ENSDARG0000003681	ZF_EIF5_DON4	AATTTAATACTCACATGTCGGAGGC	This study
IG438	<i>spata5</i>	ENSDARG00000104869	ZF_SPATA5_ACC16	GACCACCAATATCACTCCACTTCAC	This study
IG438	<i>spata5</i>	ENSDARG00000104869	ZF_SPATA5_ATG	CTTTTCTTACTGGATGACATGATGC	This study
HI020	<i>tbcB</i>	ENSDARG00000068404	ZF_TBCB_ATG	GATTGTCACACTCCCCTCCATCTTC	This study
HI020	<i>tbcB</i>	ENSDARG00000068404	ZF_TBCB_ACC6	GCCGTACCTGAAAACAATAGAAGCA	This study
HA343	<i>tnpo3</i>	ENSDARG00000045680	TNPO3_ATG	GGTTTCCCCTTCCATGGTGTCTCT	20
HA343	<i>tnpo3</i>	ENSDARG00000045680	TNPO3_SPLICE_ACC6	TCATCCCTCTGCTTCAATGACGAGT	20
IM087	<i>ube3d</i>	ENSDARG00000026178	ZF_UBE3D_ACC9	CAACACTACACATCAGGGAAAAACA	This study
IM087	<i>ube3d</i>	ENSDARG00000026178	ZF_UBE3D_ATG	TCGCAGTCTTCCATTGGTATTTTC	This study
IL015	<i>unc45a</i>	ENSDARG00000103643	ZF_UNC45A_ACC2/ATG	CTGGGACATCTACACAGTCAGAAAA	This study
HJ028	<i>upf1</i>	ENSDARG00000016302	ZF_UPF1_ACC2	GTTACCTGAAAACAAGATGAGCAA	91
JZ007	<i>yeats2</i>	ENSDARG00000078767	ZF_YEATS2_DON25	AGAAACTGGCACACACTTACCTGGT	This study
JZ007	<i>yeats2</i>	ENSDARG00000078767	ZF_YEATS2_ACC23	CCGTGCTGAGGGGAGATTGATAATAA	This study

<sup>a</sup> Zv10

<sup>b</sup> Morpholinos target translation initiation codon (ATG) or splice sites (*DON* donor, *ACC* acceptor, numbers refer to exons)

**Supplementary Table 4 | Genotyping primers used in this study.**

Affected Gene	Primer	Type
<i>fli1a</i>	ATTTCTCAGGCTCTCCAACAG	Forward
	TAGCAAGTCGACTGCTGGTG	Reverse
<i>pole</i>	GTCTGTGGACATTTGATGCTTG	Forward
	GACTCCAGCTTGGACCCAC	Reverse
<i>tbcB</i>	ATGAGGAAGAGAGGGCCAAG	Forward
	CCACTGCTGTTAGGTACATC	Reverse
<i>unc45a</i>	GGGAGCCAAATAGTATTCAAG	Forward
	GCGGTACAGGACTGCACTCT	Reverse
<i>pnrc1</i>	CATAGACAAGACATCACCTG	Forward
	TGCTTCAGGATGTTTTCTGG	Reverse
<i>ube3d</i>	TGGATGTGTGGGAGAAGGAC	Forward
	TCAGAGTGGTGTGTGACCTG	Reverse
<i>naa50</i>	TGCACTGCTGGTTTACGGTG	Mutant
	TTAGGCTCTGTGTTGCATGTG	Mutant
	GTCAGTTCACAGCTAGTTGAC	Wildtype
	GTTGAGTTACGGCTTTGTTGTG	Wildtype
<i>yeats2</i>	GTCAAAGTAGAACAGGGC	Forward
	ATCCCTCTGATTGTCCC	Reverse
<i>atad5a</i>	GACAGGCTCTTCAGTGTGTC	Forward
	CAGCTTCAAGAGCAAGTCTCTG	Reverse
<i>anapc1</i>	CAGCAGGGCGACTCATTTTG	Forward
	CTGAACTGGGCTGTGCACTG	Reverse
<i>nek7</i>	CAATTGAACCACCCCAATGT	Forward
	AATGGGCATGTGTCCTTACC	Reverse
<i>spata5</i>	GTCCGCAGGGTCCAGAGTTAC	Forward
	TGACGGAGCAACAGTTCTGG	Reverse
<i>mat2aa</i>	CCCAACTAACCAAGCCAAGTT	Forward
	AGTCTCGCTAGTGGCATAAC	Reverse
<i>nol9</i>	CCAACAGTGTCTTCAGAACG	Forward
	ATGTGGATTGGACCTGGAAAC	Reverse
<i>EIF5</i>	GCTCTAAATAGGCCCTCCGACA	Forward
	CAGTGCATCAAGGGTACACAG	Reverse
<i>pi4kaa</i>	AAGGTGGAGTGTGCTTTAAG	Forward
	CGTGACAGTGTGTTCTTCAG	Reverse
<i>pip5k1ba</i>	ACTGAAACACAATCAAGCAAGTG	Forward
	CTGTTGCTAAAGACATGTTGTG	Reverse

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**Additional information**

**Supplementary information** The online version contains supplementary material available at <https://doi.org/10.1038/s42003-024-05841-2>.



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